

FIG. 1

## DNA and Predicted primary amino acid sequence of GFP (Hind3-EcoR1 fragment).

5' - AAGCTTT

ATG MET	AGT SER	AAA LYS	GGA GLY	GAA GLU	GAA GLU	CTT LEU	TTC PHE	ACT THR	GGA GLY	GTT VAL	GTC VAL	CCA PRO	ATT ILE	CTT LEU	GTT VAL	GAA GLU	TTA LEU	GAT ASP	CGC GLY
GAT ASP	GTT VAL	AAT ASN	GGG GLY	CAA GLN	AAA LYS	TTC PHE	TCT SER	GTT VAL	AGT SER	GGA GLY	GAG GLU	GGT GLY	GAA GLU	GGT GLY	GAT ASP	GCA ALA	ACA THR	TAC TYR	GGA GLY
AAA LYS	CTT LEU	ACC THR	CTT LEU	AAA LYS	TTT PHE	ATT ILE	TGC CYS	ACT THR	ACT THR	GGG GLY	AAG LYS	CTA LEU	CCT PRO	GTT VAL	CCA PRO	TGG TRP	CCA PRO	ACG THR	CTT LEU
GTC VAL	ACT THR	ACT THR	TTC PHE	TCT SER	TAT TYR	GGT GLY	GTT VAL	CAA GLN	TGC CYS	TTT PHE	TCA SER	AGA ARG	TAC TYR	CCA PRO	GAT ASP	CAT HIS	ATG MET	AAA LYS	CAG GLN
CAT HIS	GAC ASP	TTT PHE	TTC PHE	AAG LYS	AGT SER	GCC ALA	ATG MET	CCC PRO	GAA GLU	GGT GLY	TAT TYR	GTA VAL	CAG GLN	GAA GLU	AGA ARG	ACT THR	ATA ILE	TTT PHE	TAC TYR
AAA LYS	GAT ASP	GAC ASP	GGG GLY	AAC ASN	TAC TYR	AAG LYS	ACA THR	CGT ARG	GCT ALA	GAA GLU	GTC VAL	AAG LYS	TTT PHE	GAA GLU	GGT GLY	GAT ASP	ACC THR	CTT LEU	GTT VAL
AAT ASN	AGA ARG	ATC ILE	GAG GLU	TTA LEU	AAA LYS	GGT GLY	ATT ILE	GAT ASP	TTT PHE	AAA LYS	GAA GLU	GAT ASP	GGA GLY	AAC ASN	ATT ILE	CTT LEU	GGA GLY	CAC HIS	AAA LYS
ATG MET	GAA GLU	TAC TYR	AAT ASN	TAT TYR	AAC ASN	TCA SER	CAC HIS	AAT ASN	GTA VAL	TAC TYR	ATC ILE	ATG MET	GCA ALA	GAC ASP	AAA LYS	CCA PRO	AAG LYS	AAT ASN	GGA GLY
ATC ILE	AAA LYS	GTT VAL	AAC ASN	TTC PHE	AAA LYS	ATT ILE	AGA ARG	CAC HIS	AAC ASN	ATT ILE	AAA LYS	GAT ASP	GGA GLY	AGC SER	GTT VAL	CAA GLN	TTA LEU	GCA ALA	GAC ASP
CAT HIS	TAT TYR	CAA GLN	CAA GLN	AAT ASN	ACT THR	CCA PRO	ATT ILE	GGC GLY	GAT ASP	GGC GLY	CCT PRO	GTC VAL	CTT LEU	TTA LEU	CCA PRO	GAC ASP	AAC ASN	CAT HIS	TAC TYR
CTG LEU	TCC SER	ACG THR	CAA GLN	TCT SER	GCC ALA	CTT LEU	TCC SER	AAA LYS	GAT ASP	CCC PRO	AAC ASN	GAA GLU	AAG LYS	AGA ARG	GAT ASP	CAC HIS	ATG MET	ATC ILE	CTT LEU
CTT LEU	GAG GLU	TTT PHE	GTA VAL	ACA THR	GCT ALA	GCT ALA	GGG GLY	ATT ILE	ACA THR	CAT HIS	GGC GLY	ATG MET	GAT ASP	GAA GLU	CTA LEU	TAC TYR	AAA LYS	TAA	

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Nucleotide sequence (764bp) of GFP (Hind3-EcoR1 fragment)

AAGCTTTATGAGTAAAGGAGAAGAACTTTTCACTGGAGTT  
GTCCCAATTCTTGTTGAATTAGATGGCGATGTTAATGGGC  
AAAAATTCTCTGTTAGTGGAGAGGGTGAAGGTGATGCAAC  
ATACGGAAAACCTTACCCTTAAATTTATTTGCACTACTGGG  
AAGCTACCTGTTCCATGGCCAACGCTTGTCCTACTTTCT  
CTTATGGTGTTCATGCTTTTCAAGATACCCAGATCATAT  
GAAACAGCATGACTTTTTCAAGAGTGCCATGCCCCGAAGGT  
TATGTACAGGAAAGAACTATATTTTACAAAGATGACGGGA  
ACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATAC  
CCTTGTTAATAGAATCGAGTTAAAAGGTATTGATTTTAAA  
GAAGATGGAAACATTCTTGACACAAAATGGAATACAAC  
ATAACTCACATAATGTATACATCATGGCAGACAAACCAA  
GAATGGCATCAAAGTTAACTTCAAATTAGACACAACATT  
AAAGATGGAAGCGTTCAATTAGCAGACCATTATCAACAAA  
ATACTCCAATTGGCGATGGCCCTGTCCTTTTACCAGACAA  
CCATTACCTGTCCACGCAATCTGCCCTTTCCAAAGATCCC  
AACGAAAAGAGAGATCACATGATCCTTCTTGAGTTTGTA  
CAGCTGCTGGGATTACACATGGCATGGATGAACTATACAA  
ATAAATGTCCAGACTTCCAATTGACACTAAAGGGATCCGA  
ATTC

Fig. 2b

090316.060401

## DNA and predicted primary amino acid sequence of F64L-Y66H-GFP (Hind3-EcoR1 fragment).

5' - AAGCTTT

ATG	AGT	AAA	GGA	GAA	GAA	CTT	TTC	ACT	GGA	GTT	GTC	CCA	ATT	CTT	GTT	GAA	TTA	GAT	GGC
MET	SER	LYS	GLY	GLU	GLU	LEU	PHE	THR	GLY	VAL	VAL	PRO	ILE	LEU	VAL	GLU	LEU	ASP	GLY
GAT	GTT	AAT	GGG	CAA	AAA	TTC	TCC	GTT	AGT	GGA	GAG	GGT	GAA	GGT	GAT	GCA	ACA	TAC	GGA
ASP	VAL	ASN	GLY	GLN	LYS	PHE	SER	VAL	SER	GLY	GLU	GLY	GLU	GLY	ASP	ALA	THR	TYR	GLY
AAA	CTT	ACC	CTT	AAA	TTT	ATT	TGC	ACT	ACT	GGG	AAG	CTA	CCT	GTT	CCA	TGG	CCA	ACG	CTT
LYS	LEU	THR	LEU	LYS	PHE	ILE	CYS	THR	THR	GLY	LYS	LEU	PRO	VAL	PRO	TRP	PRO	THR	LEU
GTC	ACT	ACT	CTC	TCT	CAT	GGT	GTT	CAA	TGC	TTT	TCT	AGA	TAC	CCA	GAT	CAT	ATG	AAA	CAG
VAL	THR	THR	LEU	SER	HIS	GLY	VAL	GLN	CYS	PHE	SER	ARG	TYR	PRO	ASP	HIS	MET	LYS	GLN
CAT	GAC	TTT	TTC	AAG	AGT	GCC	ATG	CCC	GAA	GGT	TAT	GTA	CAG	GAA	AGA	ACT	ATA	TTT	TAC
HIS	ASP	PHE	PHE	LYS	SER	ALA	MET	PRO	GLU	GLY	TYR	VAL	GLN	GLU	ARG	THR	ILE	PHE	TYR
AAA	GAT	GAC	GGG	AAC	TAC	AAG	ACA	CGT	GCT	GAA	GTC	AAG	TTT	GAA	GGT	GAT	ACC	CTT	GTT
LYS	ASP	ASP	GLY	ASN	TYR	LYS	THR	ARG	ALA	GLU	VAL	LYS	PHE	GLU	GLY	ASP	THR	LEU	VAL
AAT	AGA	ATC	GAG	TTA	AAA	GGT	ATT	GAT	TTT	AAA	GAA	GAT	GGA	AAC	ATT	CTT	GGA	CAC	AAA
ASN	ARG	ILE	GLU	LEU	LYS	GLY	ILE	ASP	PHE	LYS	GLU	ASP	GLY	ASN	ILE	LEU	GLY	HIS	LYS
ATG	GAA	TAC	AAT	TAT	AAC	TCA	CAT	AAT	GTA	TAC	ATC	ATG	GCA	GAC	AAA	CCA	AAG	AAT	GGC
MET	GLU	TYR	ASN	TYR	ASN	SER	HIS	ASN	VAL	TYR	ILE	MET	ALA	ASP	LYS	PRO	LYS	ASN	GLY
ATC	AAA	GTT	AAC	TTC	AAA	ATT	AGA	CAC	AAC	ATT	AAA	GAT	GGA	AGC	GTT	CAA	TTA	GCA	GAC
ILE	LYS	VAL	ASN	PHE	LYS	ILE	ARG	HIS	ASN	ILE	LYS	ASP	GLY	SER	VAL	GLN	LEU	ALA	ASP
CAT	TAT	CAA	CAA	AAT	ACT	CCA	ATT	GGC	GAT	GGC	CCT	GTC	CTT	TTA	CCA	GAC	AAC	CAT	TAC
HIS	TYR	GLN	GLN	ASN	THR	PRO	ILE	GLY	ASP	GLY	PRO	VAL	LEU	LEU	PRO	ASP	ASN	HIS	TYR
CTG	TCC	ACG	CAA	TCT	GCC	CTT	TCC	AAA	GAT	CCC	AAC	GAA	AAG	AGA	GAT	CAC	ATG	ATC	CTT
LEU	SER	THR	GLN	SER	ALA	LEU	SER	LYS	ASP	PRO	ASN	GLU	LYS	ARG	ASP	HIS	MET	ILE	LEU
CTA	GAG	TTT	GTA	ACA	GCT	GCT	GGG	ATT	ACA	CAT	GGC	ATG	GAT	GAA	CTA	TAC	AAA	TAA	
LEU	GLU	PHE	VAL	THR	ALA	ALA	GLY	ILE	THR	HIS	GLY	MET	ASP	GLU	LEU	TYR	LYS		

ATGTCAGACTTCCAATTGACACTAAAGGGATCCGAATTC - 3'

Fig. 3

## DNA and predicted primary amino acid sequence of F64L-GFP (Hind3 – EcoR1 fragment).

5' - AAGCTTT

ATG	AGT	AAA	GGA	GAA	GAA	CTT	TTC	ACT	GGA	GTT	GTC	CCA	ATT	CTT	GTT	GAA	TTA	GAT	GGC
MET	SER	LYS	GLY	GLU	GLU	LEU	PHE	THR	GLY	VAL	VAL	PRO	ILE	LEU	VAL	GLU	LEU	ASP	GLY
GAT	GTT	AAT	GGG	CAA	AAA	TTC	TCT	GTT	AGT	GGA	GAG	GGT	GAA	GGT	GAT	GCA	ACA	TAC	GGA
ASP	VAL	ASN	GLY	GLN	LYS	PHE	SER	VAL	SER	GLY	GLU	GLY	GLU	GLY	ASP	ALA	THR	TYR	GLY
AAA	CTT	ACC	CTT	AAA	TTT	ATT	TGC	ACT	ACT	GGG	AAG	CTA	CCT	GTT	CCA	TGG	CCA	ACG	CTT
LYS	LEU	THR	LEU	LYS	PHE	ILE	CYS	THR	THR	GLY	LYS	LEU	PRO	VAL	PRO	TRP	PRO	THR	LEU
GTC	ACT	ACT	CTC	TCT	TAT	GGT	GTT	CAA	TGC	TTT	TCT	AGA	TAC	CCA	GAT	CAT	ATG	AAA	CAG
VAL	THR	THR	LEU	SER	TYR	GLY	VAL	GLN	CYS	PHE	SER	ARG	TYR	PRO	ASP	HIS	MET	LYS	GLN
CAT	GAC	TTT	TTC	AAG	AGT	GCC	ATG	CCC	GAA	GGT	TAT	GTA	CAG	GAA	AGA	ACT	ATA	TTT	TAC
HIS	ASP	PHE	PHE	LYS	SER	ALA	MET	PRO	ARG	GLY	TYR	VAL	GLN	GLU	ARG	THR	ILE	PHE	TYR
AAA	GAT	GAC	GGG	AAC	TAC	AAG	ACA	CGT	GCT	GAA	GTC	AAG	TTT	GAA	GGT	GAT	ACC	CTT	GTT
LYS	ASP	ASP	GLY	ASN	TYR	LYS	THR	ARG	ALA	GLU	VAL	LYS	PHE	GLU	GLY	ASP	THR	LEU	VAL
AAT	AGA	ATC	GAG	TTA	AAA	GGT	ATT	GAT	TTT	AAA	GAA	GAT	GGA	AAC	ATT	CTT	GGA	CAC	AAA
ASN	ARG	ILE	GLU	LEU	LYS	GLY	ILE	ASP	PHE	LYS	GLU	ASP	GLY	ASN	ILE	LEU	GLY	HIS	LYS
ATG	GAA	TAC	AAT	TAT	AAC	TCA	CAT	AAT	GTA	TAC	ATC	ATG	GCA	GAC	AAA	CCA	AAG	AAT	GGC
MET	GLU	TYR	ASN	TYR	ASN	SER	HIS	ASN	VAL	TYR	ILE	MET	ALA	ASP	LYS	PRO	LYS	ASN	GLY
ATC	AAA	GTT	AAC	TTC	AAA	ATT	AGA	CAC	AAC	ATT	AAA	GAT	GGA	AGC	GTT	CAA	TTA	GCA	GAC
ILE	LYS	VAL	ASN	PHE	LYS	ILE	ARG	HIS	ASN	ILE	LYS	ASP	GLY	SER	VAL	GLN	LEU	ALA	ASP
CAT	TAT	CAA	CAA	AAT	ACT	CCA	ATT	GGC	GAT	GGC	CCT	GTC	CTT	TTA	CCA	GAC	AAC	CAT	TAC
HIS	TYR	GLN	GLN	ASN	THR	PRO	ILE	GLY	ASP	GLY	PRO	VAL	LEU	LEU	PRO	ASP	ASN	HIS	TYR
CTG	TCC	ACG	CAA	TCT	GCC	CTT	TCC	AAA	GAT	CCC	AAC	GAA	AAG	AGA	GAT	CAC	ATG	ATC	CTT
LEU	SER	THR	GLN	SER	ALA	LEU	SER	LYS	ASP	PRO	ASN	GLU	LYS	ARG	ASP	HIS	MET	ILE	LEU
CTT	GAG	TTT	GTA	ACA	GCT	GCT	GGG	ATT	ACA	CAT	GGC	ATG	GAT	GAA	CTA	TAC	AAA	TAA	
LEU	GLU	PHE	VAL	THR	ALA	ALA	GLY	ILE	THR	HIS	GLY	MET	ASP	GLU	LEU	TYR	LYS		

ATGTCAGACTTCCAATTGACACTAAAGGGATCCGAATTC - 3'

Fig. 4

F064-060101

DNA and predicted primary amino acid sequence of F64L-S65T-GFP (Hind3 – EcoR1 fragment).

5' - AAGCTTT

ATG	AGT	AAA	GGA	GAA	GAA	CTT	TTC	ACT	GGA	GTT	GTC	CCA	ATT	CTT	GTT	GAA	TTA	GAT	GGC
MET	SER	LYS	GLY	GLU	GLU	LEU	PHE	THR	GLY	VAL	VAL	PRO	ILE	LEU	VAL	GLU	LEU	ASP	GLY
GAT	GTT	AAT	GGG	CAA	AAA	TTC	TCT	GTT	AGT	GGA	GAG	GGT	GAA	GGT	GAT	GCA	ACA	TAC	GGA
ASP	VAL	ASN	GLY	GLN	LYS	PHE	SER	VAL	SER	GLY	GLU	GLY	GLU	GLY	ASP	ALA	THR	TYR	GLY
AAA	CTT	ACC	CTT	AAA	TTT	ATT	TGC	ACT	ACT	GGG	AAG	CTA	CCT	GTT	CCA	TGG	CCA	ACG	CTT
LYS	LEU	THR	LEU	LYS	PHE	ILE	CYS	THR	THR	GLY	LYS	LEU	PRO	VAL	PRO	TRP	PRO	THR	LEU
GTC	ACT	ACT	CTC	ACT	TAT	GGT	GTT	CAA	TGC	TTT	TCT	AGA	TAC	CCA	GAT	CAT	ATG	AAA	CAG
VAL	THR	THR	LEU	THR	TYR	GLY	VAL	GLN	CYS	PHE	SER	ARG	TYR	PRO	ASP	HIS	MET	LYS	GLN
CAT	GAC	TTT	TTC	AAG	AGT	GCC	ATG	CCC	GAA	GGT	TAT	GTA	CAG	GAA	AGA	ACT	ATA	TTT	TAC
HIS	ASP	PHE	PHE	LYS	SER	ALA	MET	PRO	GLU	GLY	TYR	VAL	GLN	GLU	ARG	THR	ILE	PHE	TYR
AAA	GAT	GAC	GGG	AAC	TAC	AAG	ACA	CGT	GCT	GAA	GTC	AAG	TTT	GAA	GGT	GAT	ACC	CTT	GTT
LYS	ASP	ASP	GLY	ASN	TYR	LYS	THR	ARG	ALA	GLU	VAL	LYS	PHE	GLU	GLY	ASP	THR	LEU	VAL
AAT	AGA	ATC	GAG	TTA	AAA	GGT	ATT	GAT	TTT	AAA	GAA	GAT	GGA	AAC	ATT	CTT	GGA	CAC	AAA
ASN	ARG	ILE	GLU	LEU	LYS	GLY	ILE	ASP	PHE	LYS	GLU	ASP	GLY	ASN	ILE	LEU	GLY	HIS	LYS
ATG	GAA	TAC	AAT	TAT	AAC	TCA	CAT	AAT	GTA	TAC	ATC	ATG	GCA	GAC	AAA	CCA	AAG	AAT	GGC
MET	GLU	TYR	ASN	TYR	ASN	SER	HIS	ASN	VAL	TYR	ILE	MET	ALA	ASP	LYS	PRO	LYS	ASN	GLY
ATC	AAA	GTT	AAC	TTC	AAA	ATT	AGA	CAC	AAC	ATT	AAA	GAT	GGA	AGC	GTT	CAA	TTA	GCA	GAC
ILE	LYS	VAL	ASN	PHE	LYS	ILE	ARG	HIS	ASN	ILE	LYS	ASP	GLY	SER	VAL	GLN	LEU	ALA	ASP
CAT	TAT	CAA	CAA	AAT	ACT	CCA	ATT	GGC	GAT	GGC	CCT	GTC	CTT	TTA	CCA	GAC	AAC	CAT	TAC
HIS	TYR	GLN	GLN	ASN	THR	PRO	ILE	GLY	ASP	GLY	PRO	VAL	LEU	LEU	PRO	ASP	ASN	HIS	TYR
ATG	TCC	ACG	CAA	TCT	GCC	CTT	TCC	AAA	GAT	CCC	AAC	GAA	AAG	AGA	GAT	CAC	ATG	ATC	CTT
LEU	SER	THR	GLN	SER	ALA	LEU	SER	LYS	ASP	PRO	ASN	GLU	LYS	ARG	ASP	HIS	MET	ILE	LEU
GTT	GAG	TTT	GTA	ACA	GCT	GCT	GGG	ATT	ACA	CAT	GGC	ATG	GAT	GAA	CTA	TAC	AAA	TAA	
LEU	GLU	PHE	VAL	THR	ALA	ALA	GLY	ILE	THR	HIS	GLY	MET	ASP	GLU	LEU	TYR	LYS		

ATGTCCAGACTTCCAATTGACACTAAAGGGATCCGAATTC - 3'

5'-AAGCTTT-3'

Fig. 5

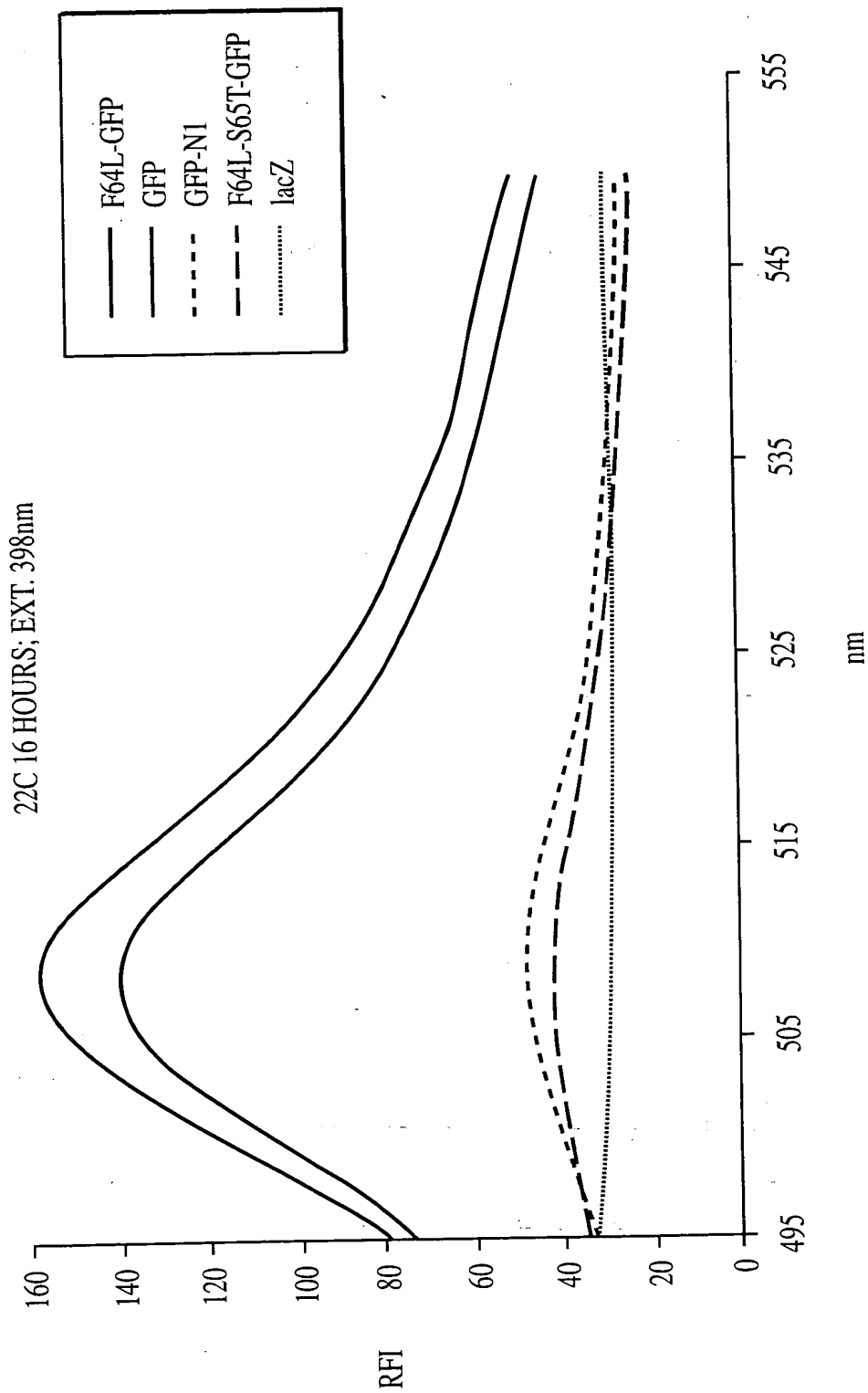


FIG. 6A

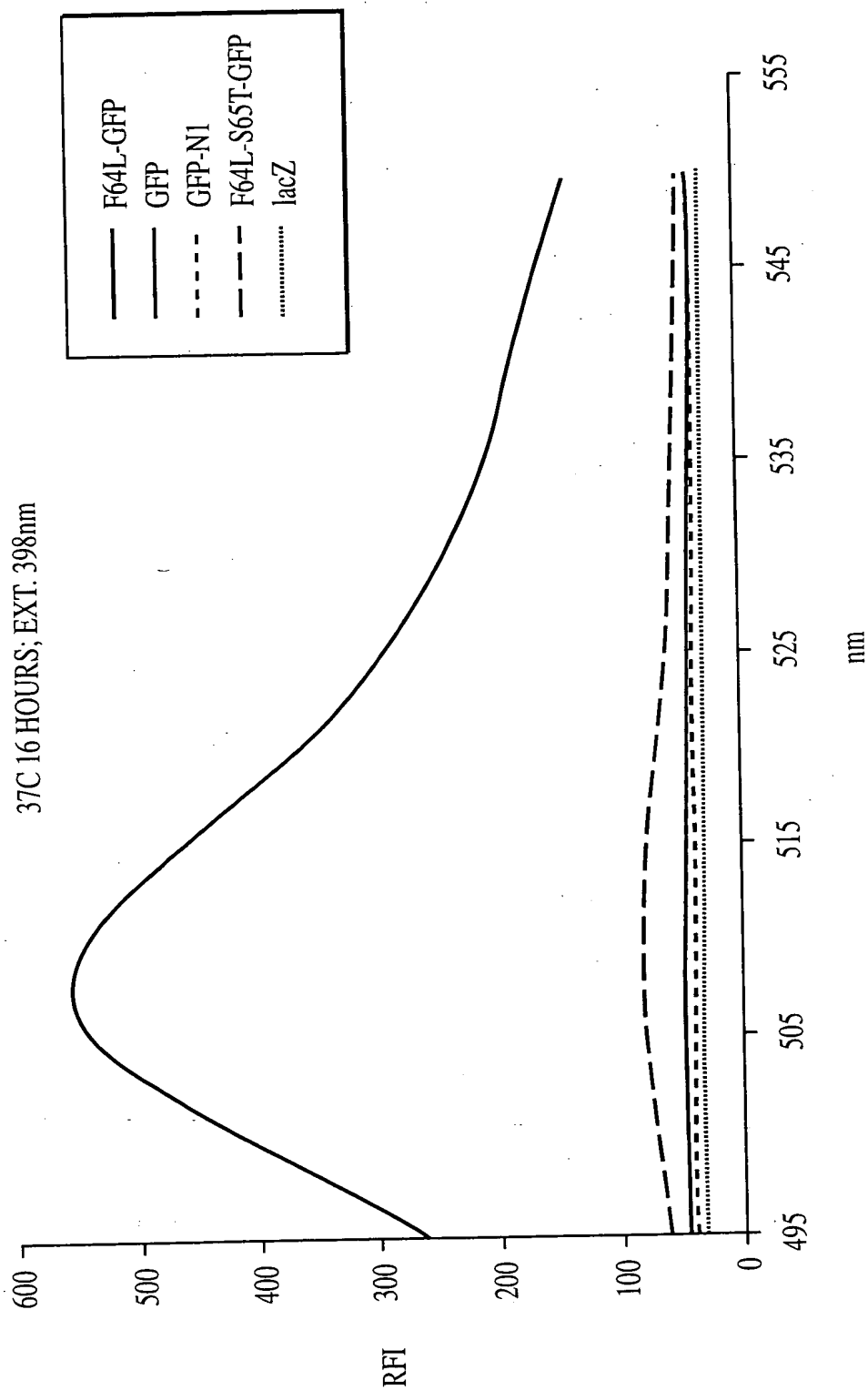


FIG. 6B



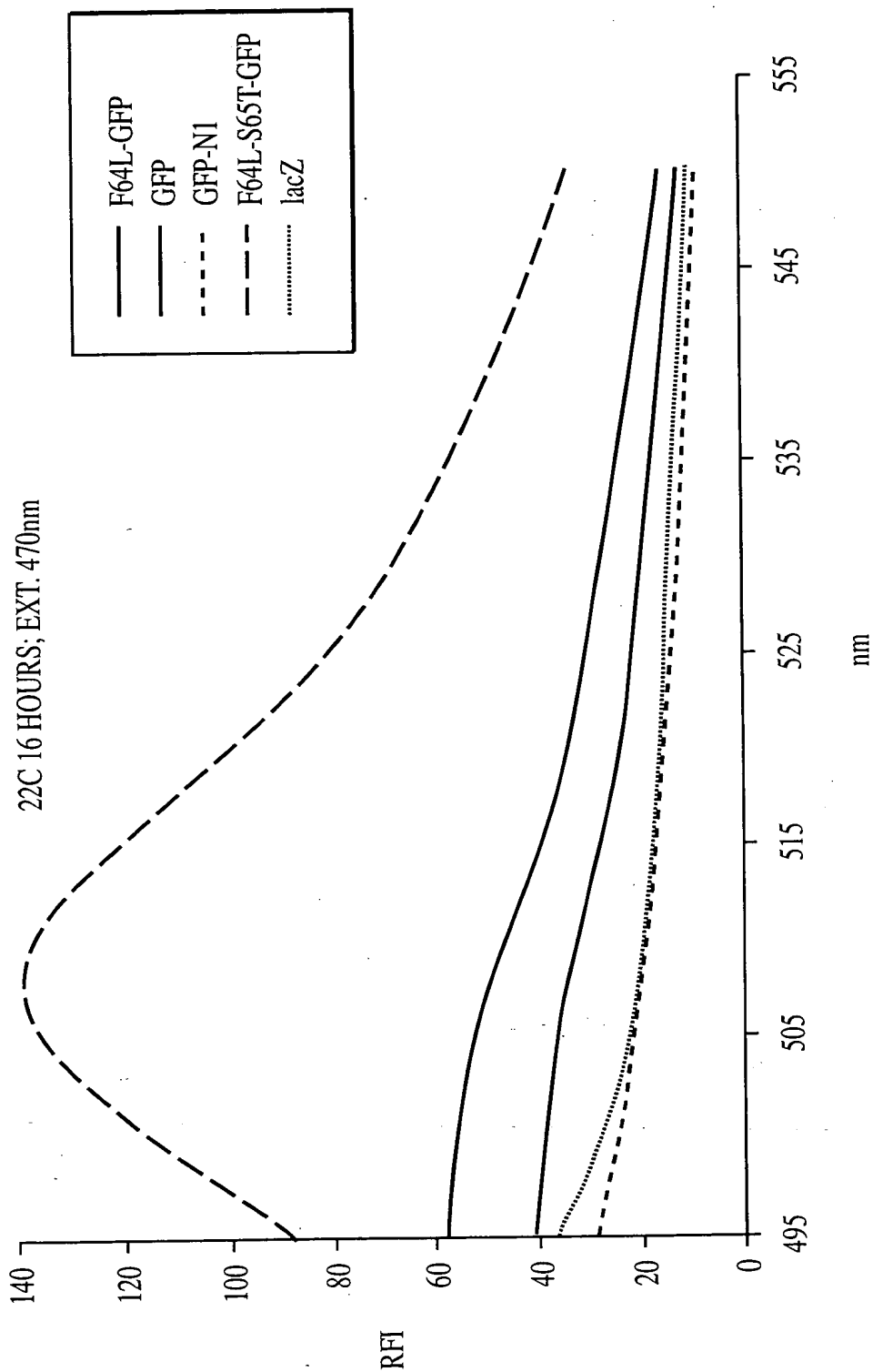


FIG. 6C

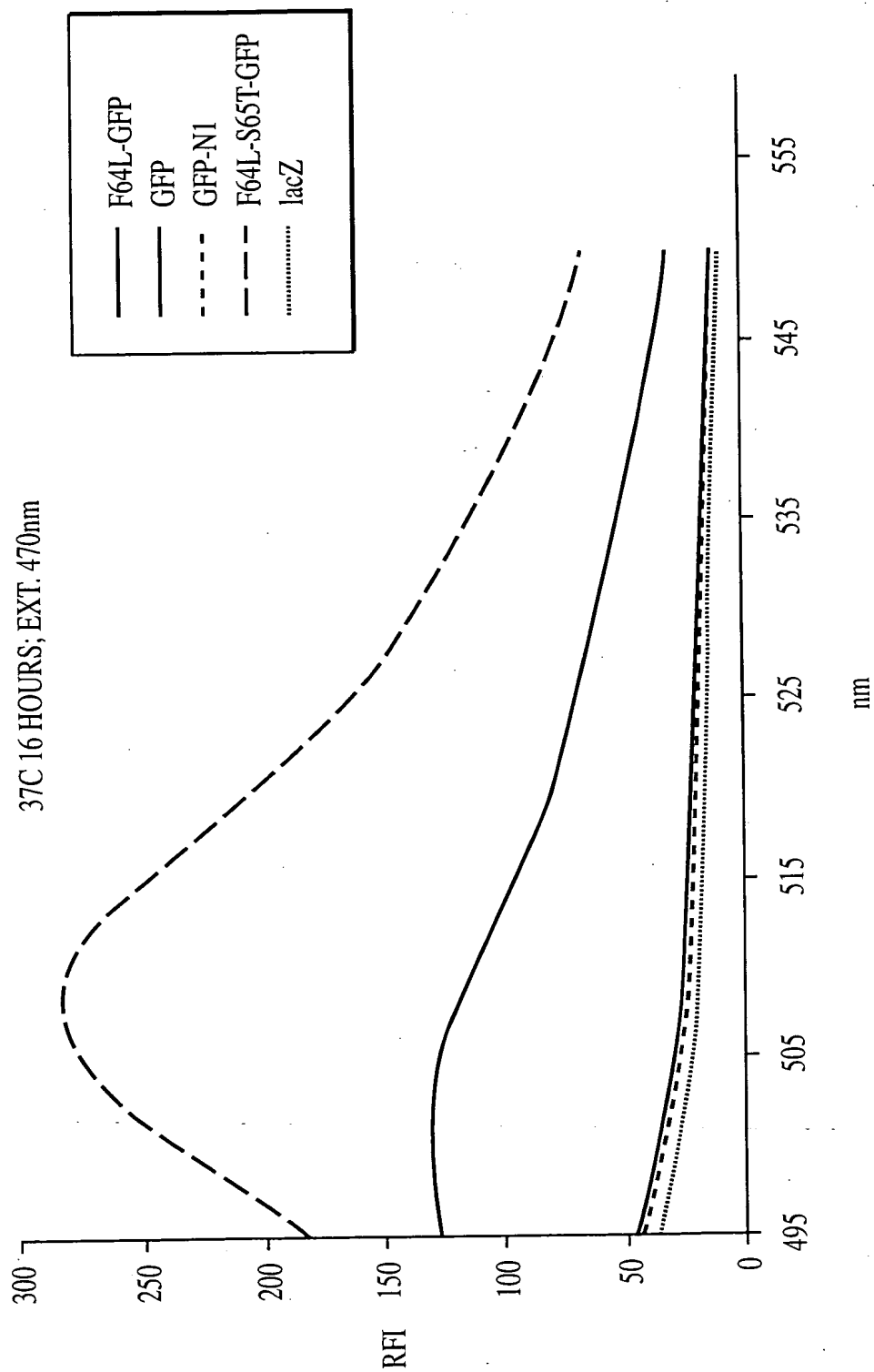


FIG. 6D

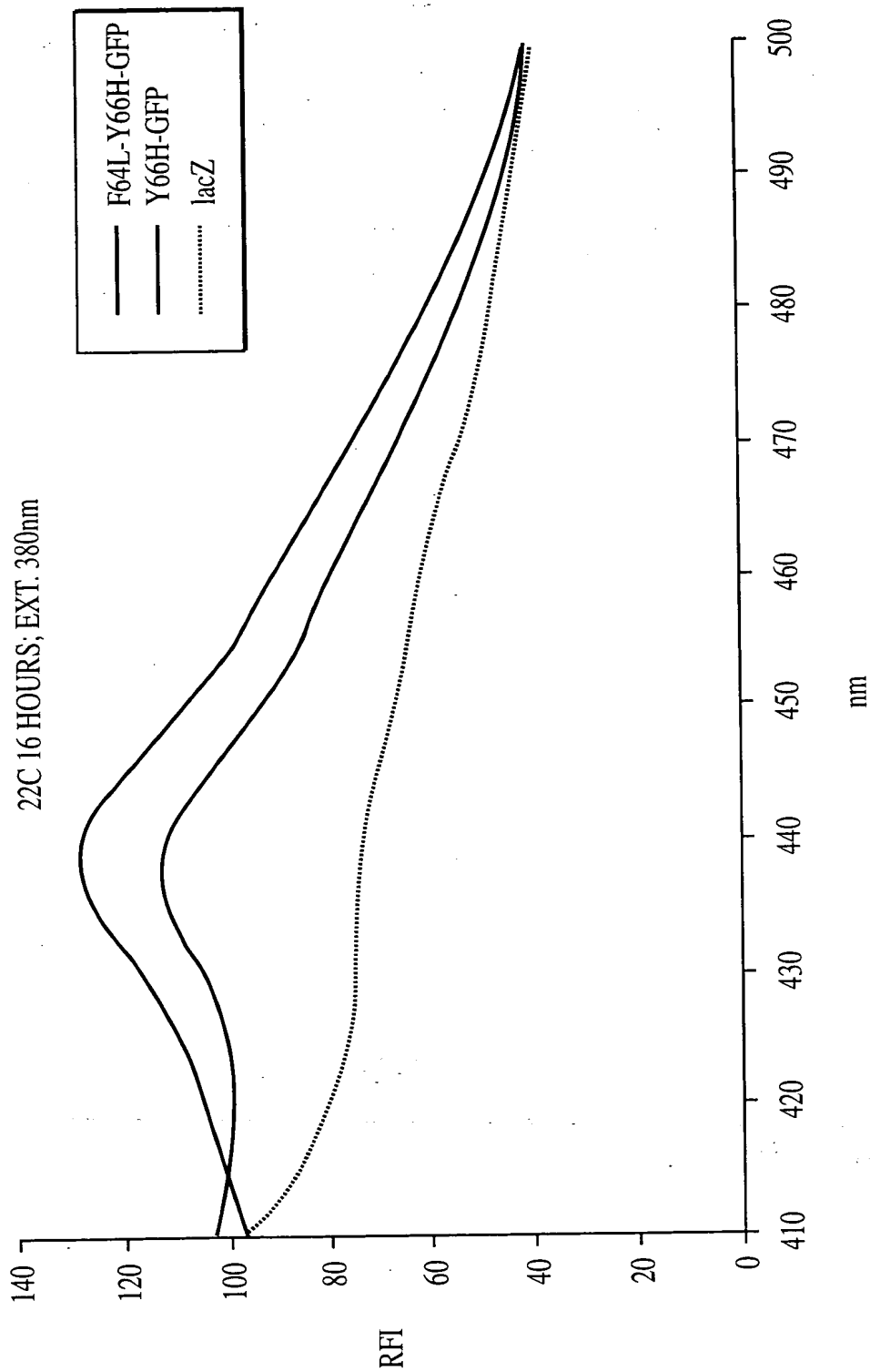


FIG. 6E

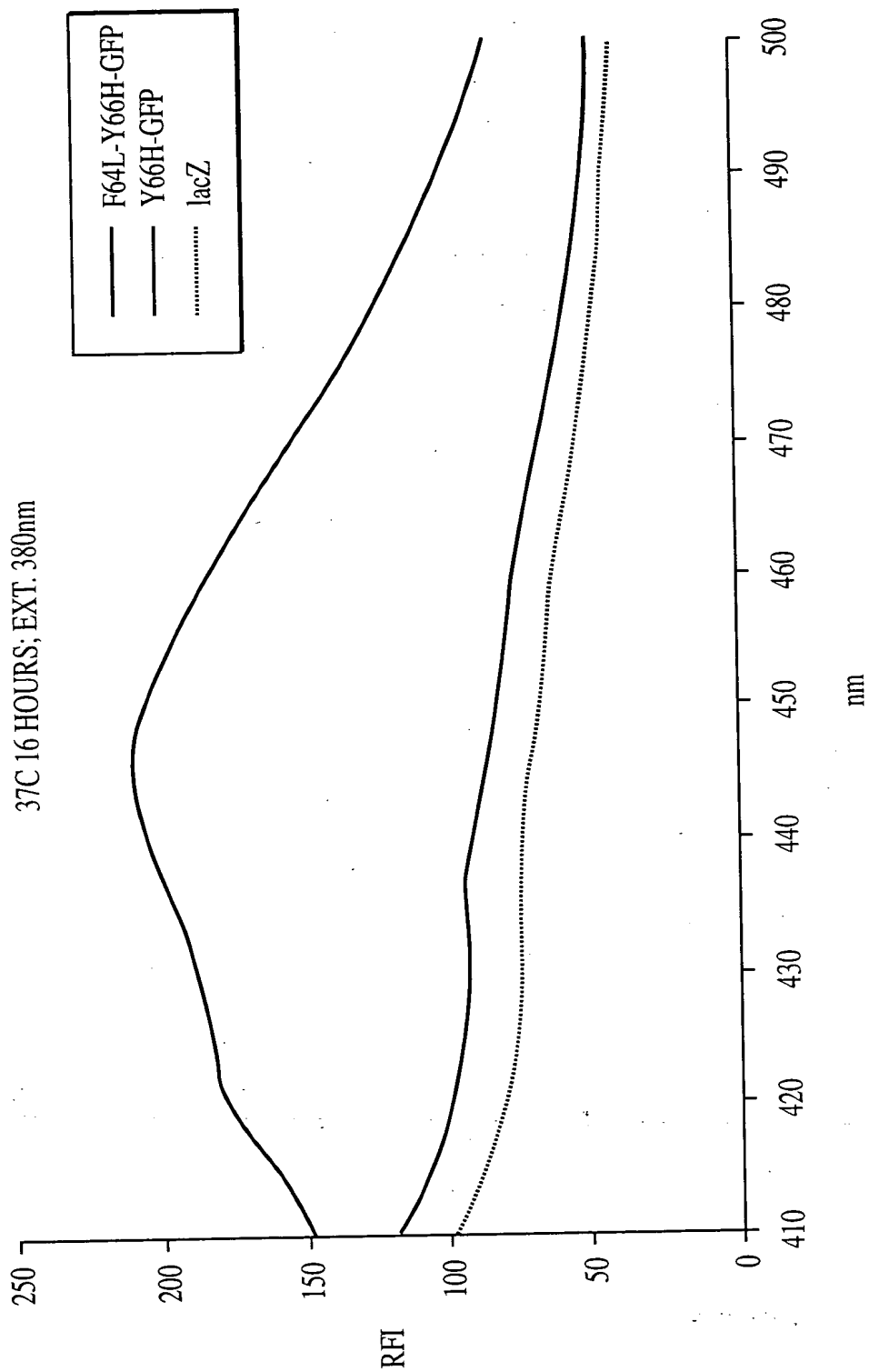


FIG. 6F